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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Kaufman, Randal J.
Wasley, Louise
- (ii) TITLE OF INVENTION: Method of Increasing Yield of Mature Proteins
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Genetics Institute, Inc.
 - (B) STREET: 87 CambridgePark Drive
 - (C) CITY: Cambridge
 - (D) STATE: Massachusetts
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 02140
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/621,092
 - (B) FILING DATE: 26-NOV-1990
 - (C) CLASSIFICATION: 424
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Kapinos, Ellen J.
 - (B) REGISTRATION NUMBER: 32,245
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617)876-1170
 - (B) TELEFAX: (617)876-5851

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2385 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..2382

(x) PUBLICATION INFORMATION:

(A) AUTHORS: van den Ouweland, A.M.W.
(C) JOURNAL: Nucleic Acids Res.
(D) VOLUME: 18
(F) PAGES: 664-
(G) DATE: 1990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG	GAG	CTC	AGG	CCC	TGG	TTC	CTA	TGG	GTC	GTA	CCA	CCA	ACA	GGA	ACC	48
Met	Glu	Leu	Arg	Pro	Trp	Phe	Leu	Trp	Val	Val	Pro	Pro	Thr	Gly	Thr	
1				5					10					15		
TTG	GTC	CTG	CTA	GCA	GCT	GAT	GCT	CAG	GGC	CAG	AAG	GTC	TTC	ACC	AAC	96
Leu	Val	Leu	Leu	Ala	Ala	Asp	Ala	Gln	Gly	Gln	Lys	Val	Phe	Thr	Asn	
			20					25					30			
ACG	TGG	GCT	GTG	CGC	ATC	CCT	GGA	GGC	CCA	GCG	GTG	GCC	AAC	AGT	GTG	144
Thr	Trp	Ala	Val	Arg	Ile	Pro	Gly	Gly	Pro	Ala	Val	Ala	Asn	Ser	Val	
		35					40					45				
GCA	CGG	AAG	CAT	GGG	TTC	CTC	AAC	CTG	GGC	CAG	ATC	TTC	GGG	GAC	TAT	192
Ala	Arg	Lys	His	Gly	Phe	Leu	Asn	Leu	Gly	Gln	Ile	Phe	Gly	Asp	Tyr	
	50					55					60					
TAC	CAC	TTC	TGG	CAT	CGA	GGA	GTG	ACG	AAG	CGG	TCC	CTG	TCG	CCT	CAC	240
Tyr	His	Phe	Trp	His	Arg	Gly	Val	Thr	Lys	Arg	Ser	Leu	Ser	Pro	His	
	65				70					75					80	
CGC	CCG	CGG	CAC	AGC	CGG	CTG	CAG	AGG	GAG	CCT	CAA	GTA	CAG	TGG	CTG	288
Arg	Pro	Arg	His	Ser	Arg	Leu	Gln	Arg	Glu	Pro	Gln	Val	Gln	Trp	Leu	
				85					90					95		
GAA	CAG	CAG	GTG	GCA	AAG	CGA	CGG	ACT	AAA	CGG	GAC	GTG	TAC	CAG	GAG	336
Glu	Gln	Gln	Val	Ala	Lys	Arg	Arg	Thr	Lys	Arg	Asp	Val	Tyr	Gln	Glu	
			100					105					110			
CCC	ACA	GAC	CCC	AAG	TTT	CCT	CAG	CAG	TGG	TAC	CTG	TCT	GGT	GTC	ACT	384
Pro	Thr	Asp	Pro	Lys	Phe	Pro	Gln	Gln	Trp	Tyr	Leu	Ser	Gly	Val	Thr	
		115					120					125				
CAG	CGG	GAC	CTG	AAT	GTG	AAG	GCG	GCC	TGG	GCG	CAG	GGC	TAC	ACA	GGG	432
Gln	Arg	Asp	Leu	Asn	Val	Lys	Ala	Ala	Trp	Ala	Gln	Gly	Tyr	Thr	Gly	
	130					135					140					
CAC	GGC	ATT	CTG	GTC	TCC	ATT	CTG	GAC	GAT	GGC	ATC	GAG	AAG	AAC	CAC	480
His	Gly	Ile	Leu	Val	Ser	Ile	Leu	Asp	Asp	Gly	Ile	Glu	Lys	Asn	His	
145					150					155					160	

CCC Pro	GAC Asp	TTG Leu	GCA Ala	GGC Gly 165	AAT Asn	TAT Tyr	GAT Asp	CCT Pro	GGG Gly 170	GCC Ala	AGT Ser	TTT Phe	CAT His	GTC Val 175	AAT Asn	528
GAC Asp	CAG Gln	GAC Asp	CCT Pro 180	GAC Asp	CCC Pro	CAG Gln	CCT Pro	CGG Arg 185	TAC Tyr	ACA Thr	CAG Gln	ATG Met	AAT Asn 190	GAC Asp	AAC Asn	576
AGG Arg	CAC His	GGC Gly 195	ACA Thr	CGG Arg	TGT Cys	GCG Ala	GGG Gly 200	GAA Glu	GTG Val	GCT Ala	GCC Ala	GTG Val 205	GCC Ala	AAC Asn	AAC Asn	624
CGT Arg 210	GTC Val	TGT Cys	GGT Gly	GTA Val	GGT Gly 215	GTG Val	GCC Ala	TAC Tyr	AAC Asn	GCC Ala	CGC Arg 220	ATT Ile	GGA Gly	GGG Gly	GTC Val	672
CGC Arg 225	ATG Met	CTG Leu	GAT Asp	GGC Gly	GAG Glu 230	GTG Val	ACA Thr	GAT Asp	GCA Ala 235	GTG Val	GAG Glu	GCA Ala	CGC Arg	TCG Ser	CTG Leu 240	720
GGC Gly	CTG Leu	AAC Asn	CCC Pro	AAC Asn 245	CAC His	ATC Ile	CAC His	ATC Ile	TAC Tyr 250	AGT Ser	GCC Ala	AGC Ser	TGG Trp	GGC Gly 255	CCC Pro	768
GAG Glu	GAT Asp	GAC Asp	GGC Gly 260	AAG Lys	ACA Thr	GTG Val	GAT Asp	GGG Gly 265	CCA Pro	GCC Ala	CGG Arg	CTC Leu	GCC Ala 270	GAG Glu	GAG Glu	816
GCC Ala	TTC Phe	TTC Phe 275	CGT Arg	GGG Gly	CTT Leu	AGC Ser	CAG Gln 280	GGC Gly	CGA Arg	GGG Gly	GGG Gly	CTG Leu 285	GGC Gly	TCC Ser	ATC Ile	864
TTT Phe 290	GTC Val	TGG Trp	GCC Ala	TCG Ser	GGG Gly	AAC Asn 295	GGG Gly	GGG Gly	CGG Arg	GAA Glu	CAT His 300	GAC Asp	AGC Ser	TGC Cys	AAC Asn	912
TGC Cys 305	GAC Asp	GGC Gly	TAC Tyr	ACC Thr	AAC Asn 310	AGT Ser	ATC Ile	TAC Tyr	ACG Thr	CTG Leu 315	TCC Ser	ATC Ile	AGC Ser	AGC Ser	GCC Ala 320	960
ACG Thr	CAG Gln	TTT Phe	GGC Gly	AAC Asn 325	GTG Val	CCG Pro	TGG Trp	TAC Tyr	AGC Ser 330	GAG Glu	GCC Ala	TGC Cys	TCG Ser	TCC Ser 335	ACA Thr	1008
CTG Leu	GCC Ala	ACG Thr	ACC Thr 340	TAC Tyr	AGC Ser	AGT Ser	GGC Gly	AAC Asn 345	CAG Gln	AAT Asn	GAG Glu	AAG Lys	CAG Gln 350	ATC Ile	GTG Val	1056
ACG Thr	ACT Thr	GAC Asp 355	TTG Leu	CGG Arg	CAG Gln	AAG Lys	TGC Cys 360	ACG Thr	GAG Glu	TCT Ser	CAC His	ACG Thr 365	GGC Gly	ACC Thr	TCA Ser	1104

GCC Ala	TCT Ser	GCC Ala	CCC Pro	TTA Leu	GCA Ala	GCC Ala	GGC Gly	ATC Ile	ATT Ile	GCT Ala	CTC Leu	ACC Thr	CTG Leu	GAG Glu	GCC Ala	1152
370						375					380					
AAT Asn	AAG Lys	AAC Asn	CTC Leu	ACA Thr	TGG Trp	CGG Arg	GAC Asp	ATG Met	CAA Gln	CAC His	CTG Leu	GTG Val	GTA Val	CAG Gln	ACC Thr	1200
385					390					395					400	
TCG Ser	AAG Lys	CCA Pro	GCC Ala	CAC His	CTC Leu	AAT Asn	GCC Ala	AAC Asn	GAC Asp	TGG Trp	GCC Ala	ACC Thr	AAT Asn	GGT Gly	GTG Val	1248
				405					410					415		
GGG Gly	CGG Arg	AAA Lys	GTG Val	AGC Ser	CAC His	TCA Ser	TAT Tyr	GGC Gly	TAC Tyr	GGG Gly	CTT Leu	TTC Phe	GAC Asp	GCA Ala	GGC Gly	1296
			420					425					430			
GCC Ala	ATG Met	GTG Val	GCC Ala	CTG Leu	GCC Ala	CAG Gln	AAT Asn	TGG Trp	ACC Thr	ACA Thr	GTC Val	GCC Ala	CCC Pro	CAG Gln	CGG Arg	1344
		435					440					445				
AAG Lys	TGC Cys	ATC Ile	ATC Ile	GAC Asp	ATC Ile	CTC Leu	ACC Thr	GAG Glu	CCC Pro	AAA Lys	GAC Asp	ATC Ile	GGG Gly	AAA Lys	CGG Arg	1392
	450					455					460					
CTC Leu	GAC Asp	CTC Leu	CGG Arg	AAC Asn	ACC Thr	GTG Val	ACC Thr	GCG Ala	TCC Ser	CTG Leu	GGC Gly	GAG Glu	CCC Pro	AAC Asn	CAC His	1440
465					470					475					480	
ATC Ile	ACT Thr	CGG Arg	CTG Leu	GAG Glu	CAC His	GCT Ala	CAG Gln	GCG Ala	CGG Arg	CTC Leu	ACC Thr	CTG Leu	TCC Ser	TAT Tyr	AAT Asn	1488
				485					490					495		
CGC Arg	CGT Arg	GGC Gly	GAC Asp	CTG Leu	GCC Ala	ATC Ile	CAC His	CTG Leu	GTC Val	AGC Ser	CCC Pro	ATG Met	GGC Gly	ACC Thr	CGC Arg	1536
			500					505					510			
TCC Ser	ACC Thr	CTG Leu	CTG Leu	GCA Ala	GCC Ala	AGG Arg	CCA Pro	CAT His	GAC Asp	TAC Tyr	TCC Ser	GCA Ala	GAT Asp	GGG Gly	TTT Phe	1584
		515					520					525				
AAT Asn	GAC Asp	TGG Trp	GCC Ala	TTC Phe	ATG Met	ACA Thr	ACT Thr	CAT His	TCC Ser	TGG Trp	GAT Asp	GAC Asp	GAT Asp	CCC Pro	TCT Ser	1632
	530					535					540					
GGG Gly	GAG Glu	TGG Trp	GTC Val	CTA Leu	GAG Glu	ATT Ile	GAA Glu	AAC Asn	ACC Thr	AGC Ser	GAA Glu	GCC Ala	AAC Asn	AAC Asn	TAT Tyr	1680
545					550					555					560	
GGG Gly	ACG Thr	CTG Leu	ACC Thr	AAC Asn	TCC Ser	ACC Thr	CTC Leu	GTA Val	CTC Leu	TAT Tyr	GGC Gly	ACC Thr	GCC Ala	CCT Pro	GAC Asp	1728
				565					570					575		

GGG Gly	CTC Leu	CCC Pro	GTA Val 580	CCT Pro	CCA Pro	GAA Glu	AGC Ser 585	AGT Ser	GGC Gly	TGC Cys	AAG Lys	ACC Thr	CTC Leu 590	ACG Thr	TCC Ser	1776
AGT Ser	CAG Gln	GCC Ala 595	TGT Cys	GTG Val	GTG Val	TGC Cys	GAG Glu 600	GAA Glu	GGC Gly	TTC Phe	TCC Ser	CTC Leu 605	CAC His	CAG Gln	AAG Lys	1824
AGC Ser 610	TGT Cys	GTC Val	CAG Gln	CAC His	TGC Cys	CCT Pro 615	CCA Pro	GGC Gly	TTC Phe	GCC Ala	CCC Pro 620	CAA Gln	GTC Val	CTC Leu	GAT Asp	1872
ACG Thr 625	CAC His	TAT Tyr	AGC Ser	ACC Thr	GAG Glu 630	AAT Asn	GAC Asp	GTG Val	GAG Glu	ACC Thr 635	ATC Ile	CGG Arg	GCC Ala	AGC Ser	GTC Val 640	1920
TGC Cys	GCC Ala	CCC Pro	TGC Cys 645	CAC His	GCC Ala	TCA Ser	TGT Cys	GCC Ala	ACA Thr 650	TGC Cys	CAG Gln	GGG Gly	CCG Pro	GCC Ala 655	CTG Leu	1968
ACA Thr	GAC Asp	TGC Cys	CTC Leu 660	AGC Ser	TGC Cys	CCC Pro	AGC Ser	CAC His 665	GCC Ala	TCC Ser	TTG Leu	GAC Asp	CCT Pro 670	GTG Val	GAG Glu	2016
CAG Gln	ACT Thr	TGC Cys 675	TCC Ser	CGG Arg	CAA Gln	AGC Ser	CAG Gln 680	AGC Ser	AGC Ser	CGA Arg	GAG Glu	TCC Ser 685	CCG Pro	CCA Pro	CAG Gln	2064
CAG Gln 690	CAG Gln	CCA Pro	CCT Pro	CGG Arg	CTG Leu	CCC Pro 695	CCG Pro	GAG Glu	GTG Val	GAG Glu	GCG Ala 700	GGG Gly	CAA Gln	CGG Arg	CTG Leu	2112
CGG Arg 705	GCA Ala	GGG Gly	CTG Leu	CTG Leu	CCC Pro 710	TCA Ser	CAC His	CTG Leu	CCT Pro	GAG Glu 715	GTG Val	GTG Val	GCC Ala	GGC Gly	CTC Leu 720	2160
AGC Ser	TGC Cys	GCC Ala	TTC Phe 725	ATC Ile	GTG Val	CTG Leu	GTC Val	TTC Phe	GTC Val 730	ACT Thr	GTC Val	TTC Phe	CTG Leu 735	CTC Leu	CTG Leu	2208
CAG Gln	CTG Leu	CGC Arg	TCT Ser 740	GGC Gly	TTT Phe	AGT Ser	TTT Phe	CGG Arg 745	GGG Gly	GTG Val	AAG Lys	GTG Val	TAC Tyr 750	ACC Thr	ATG Met	2256
GAC Asp	CGT Arg	GGC Gly 755	CTC Leu	ATC Ile	TCC Ser	TAC Tyr	AAG Lys 760	GGG Gly	CTG Leu	CCC Pro	CCT Pro	GAA Glu 765	GCC Ala	TGG Trp	CAG Gln	2304
GAG Glu 770	GAG Glu	TGC Cys	CCG Pro	TCT Ser	GAC Asp	TCA Ser 775	GAA Glu	GAG Glu	GAC Asp	GAG Glu	GGC Gly 780	CGG Arg	GGC Gly	GAG Glu	AGG Arg	2352

ACC GCC TTT ATC AAA GAC CAG AGC GCC CTC TGA
 Thr Ala Phe Ile Lys Asp Gln Ser Ala Leu
 785 790

2385

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 794 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Glu	Leu	Arg	Pro	Trp	Phe	Leu	Trp	Val	Val	Pro	Pro	Thr	Gly	Thr	1	5	10	15
Leu	Val	Leu	Leu	Ala	Ala	Asp	Ala	Gln	Gly	Gln	Lys	Val	Phe	Thr	Asn	20	25	30	
Thr	Trp	Ala	Val	Arg	Ile	Pro	Gly	Gly	Pro	Ala	Val	Ala	Asn	Ser	Val	35	40	45	
Ala	Arg	Lys	His	Gly	Phe	Leu	Asn	Leu	Gly	Gln	Ile	Phe	Gly	Asp	Tyr	50	55	60	
Tyr	His	Phe	Trp	His	Arg	Gly	Val	Thr	Lys	Arg	Ser	Leu	Ser	Pro	His	65	70	75	80
Arg	Pro	Arg	His	Ser	Arg	Leu	Gln	Arg	Glu	Pro	Gln	Val	Gln	Trp	Leu	85	90	95	
Glu	Gln	Gln	Val	Ala	Lys	Arg	Arg	Thr	Lys	Arg	Asp	Val	Tyr	Gln	Glu	100	105	110	
Pro	Thr	Asp	Pro	Lys	Phe	Pro	Gln	Gln	Trp	Tyr	Leu	Ser	Gly	Val	Thr	115	120	125	
Gln	Arg	Asp	Leu	Asn	Val	Lys	Ala	Ala	Trp	Ala	Gln	Gly	Tyr	Thr	Gly	130	135	140	
His	Gly	Ile	Leu	Val	Ser	Ile	Leu	Asp	Asp	Gly	Ile	Glu	Lys	Asn	His	145	150	155	160
Pro	Asp	Leu	Ala	Gly	Asn	Tyr	Asp	Pro	Gly	Ala	Ser	Phe	His	Val	Asn	165	170	175	
Asp	Gln	Asp	Pro	Asp	Pro	Gln	Pro	Arg	Tyr	Thr	Gln	Met	Asn	Asp	Asn	180	185	190	

Arg	His	Gly	Thr	Arg	Cys	Ala	Gly	Glu	Val	Ala	Ala	Val	Ala	Asn	Asn	
		195					200					205				
Arg	Val	Cys	Gly	Val	Gly	Val	Ala	Tyr	Asn	Ala	Arg	Ile	Gly	Gly	Val	
	210					215					220					
Arg	Met	Leu	Asp	Gly	Glu	Val	Thr	Asp	Ala	Val	Glu	Ala	Arg	Ser	Leu	
225					230					235					240	
Gly	Leu	Asn	Pro	Asn	His	Ile	His	Ile	Tyr	Ser	Ala	Ser	Trp	Gly	Pro	
				245					250					255		
Glu	Asp	Asp	Gly	Lys	Thr	Val	Asp	Gly	Pro	Ala	Arg	Leu	Ala	Glu	Glu	
			260					265					270			
Ala	Phe	Phe	Arg	Gly	Leu	Ser	Gln	Gly	Arg	Gly	Gly	Leu	Gly	Ser	Ile	
		275					280					285				
Phe	Val	Trp	Ala	Ser	Gly	Asn	Gly	Gly	Arg	Glu	His	Asp	Ser	Cys	Asn	
	290					295					300					
Cys	Asp	Gly	Tyr	Thr	Asn	Ser	Ile	Tyr	Thr	Leu	Ser	Ile	Ser	Ser	Ala	
305					310					315					320	
Thr	Gln	Phe	Gly	Asn	Val	Pro	Trp	Tyr	Ser	Glu	Ala	Cys	Ser	Ser	Thr	
				325					330					335		
Leu	Ala	Thr	Thr	Tyr	Ser	Ser	Gly	Asn	Gln	Asn	Glu	Lys	Gln	Ile	Val	
			340					345					350			
Thr	Thr	Asp	Leu	Arg	Gln	Lys	Cys	Thr	Glu	Ser	His	Thr	Gly	Thr	Ser	
		355					360					365				
Ala	Ser	Ala	Pro	Leu	Ala	Ala	Gly	Ile	Ile	Ala	Leu	Thr	Leu	Glu	Ala	
	370					375					380					
Asn	Lys	Asn	Leu	Thr	Trp	Arg	Asp	Met	Gln	His	Leu	Val	Val	Gln	Thr	
385					390					395					400	
Ser	Lys	Pro	Ala	His	Leu	Asn	Ala	Asn	Asp	Trp	Ala	Thr	Asn	Gly	Val	
				405					410					415		
Gly	Arg	Lys	Val	Ser	His	Ser	Tyr	Gly	Tyr	Gly	Leu	Phe	Asp	Ala	Gly	
			420					425					430			
Ala	Met	Val	Ala	Leu	Ala	Gln	Asn	Trp	Thr	Thr	Val	Ala	Pro	Gln	Arg	
		435					440					445				
Lys	Cys	Ile	Ile	Asp	Ile	Leu	Thr	Glu	Pro	Lys	Asp	Ile	Gly	Lys	Arg	
	450					455					460					
Leu	Asp	Leu	Arg	Asn	Thr	Val	Thr	Ala	Ser	Leu	Gly	Glu	Pro	Asn	His	
465					470					475					480	

Ile	Thr	Arg	Leu	Glu	His	Ala	Gln	Ala	Arg	Leu	Thr	Leu	Ser	Tyr	Asn	
				485					490					495		
Arg	Arg	Gly	Asp	Leu	Ala	Ile	His	Leu	Val	Ser	Pro	Met	Gly	Thr	Arg	
			500					505					510			
Ser	Thr	Leu	Leu	Ala	Ala	Arg	Pro	His	Asp	Tyr	Ser	Ala	Asp	Gly	Phe	
		515					520					525				
Asn	Asp	Trp	Ala	Phe	Met	Thr	Thr	His	Ser	Trp	Asp	Asp	Asp	Pro	Ser	
	530					535					540					
Gly	Glu	Trp	Val	Leu	Glu	Ile	Glu	Asn	Thr	Ser	Glu	Ala	Asn	Asn	Tyr	
545					550					555					560	
Gly	Thr	Leu	Thr	Asn	Ser	Thr	Leu	Val	Leu	Tyr	Gly	Thr	Ala	Pro	Asp	
				565					570					575		
Gly	Leu	Pro	Val	Pro	Pro	Glu	Ser	Ser	Gly	Cys	Lys	Thr	Leu	Thr	Ser	
			580					585					590			
Ser	Gln	Ala	Cys	Val	Val	Cys	Glu	Glu	Gly	Phe	Ser	Leu	His	Gln	Lys	
		595					600					605				
Ser	Cys	Val	Gln	His	Cys	Pro	Pro	Gly	Phe	Ala	Pro	Gln	Val	Leu	Asp	
	610					615					620					
Thr	His	Tyr	Ser	Thr	Glu	Asn	Asp	Val	Glu	Thr	Ile	Arg	Ala	Ser	Val	
625					630					635					640	
Cys	Ala	Pro	Cys	His	Ala	Ser	Cys	Ala	Thr	Cys	Gln	Gly	Pro	Ala	Leu	
				645					650					655		
Thr	Asp	Cys	Leu	Ser	Cys	Pro	Ser	His	Ala	Ser	Leu	Asp	Pro	Val	Glu	
			660					665					670			
Gln	Thr	Cys	Ser	Arg	Gln	Ser	Gln	Ser	Ser	Arg	Glu	Ser	Pro	Pro	Gln	
		675					680					685				
Gln	Gln	Pro	Pro	Arg	Leu	Pro	Pro	Glu	Val	Glu	Ala	Gly	Gln	Arg	Leu	
	690					695					700					
Arg	Ala	Gly	Leu	Leu	Pro	Ser	His	Leu	Pro	Glu	Val	Val	Ala	Gly	Leu	
705					710					715					720	
Ser	Cys	Ala	Phe	Ile	Val	Leu	Val	Phe	Val	Thr	Val	Phe	Leu	Leu	Leu	
				725					730					735		
Gln	Leu	Arg	Ser	Gly	Phe	Ser	Phe	Arg	Gly	Val	Lys	Val	Tyr	Thr	Met	
			740					745					750			

Asp Arg Gly Leu Ile Ser Tyr Lys Gly Leu Pro Pro Glu Ala Trp Gln
755 760 765

Glu Glu Cys Pro Ser Asp Ser Glu Glu Asp Glu Gly Arg Gly Glu Arg
770 775 780

Thr Ala Phe Ile Lys Asp Gln Ser Ala Leu
785 790